THE LANCET
Infectious Diseases

Supplementary appendix 2

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

1 # SUPPLEMENTARY APPENDIX
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4 **Definition of confirmed cases and community close contacts**
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6 **Table S1. Singapore Ministry of Health criteria for suspected cases up to April 4, 2020.**

Date	Suspect case definition
January 2, 2020 (Initial)	(a) A person with clinical signs and symptoms suggestive of <u>pneumonia</u> or <u>severe respiratory infection with breathlessness</u> AND travel to or residence in Wuhan city within the last 14 days; or (b) A person with an <u>acute respiratory illness of any degree of severity</u> who, within 14 days before onset of illness, had close contact[a] with a pneumonia case of unknown cause linked to the Wuhan cluster.
January 21, 2020	(a) A person with clinical signs and symptoms suggestive of <u>pneumonia</u> or <u>severe respiratory infection with breathlessness</u> AND travel to mainland China within 14 days before onset of illness; or (b) A person with an <u>acute respiratory illness of any degree of severity</u> who, within 14 days before onset of illness, had been to a hospital in mainland China or had close contact[a] with a case of 2019 novel coronavirus infection.
January 25, 2020	(a) A person with clinical signs and symptoms suggestive of <u>pneumonia</u> or <u>severe respiratory infection with breathlessness</u> AND travel to mainland China within 14 days before onset of illness; or (b) A person with an <u>acute respiratory illness of any degree of severity</u> who, within 14 days before onset of illness had: i. Been to Wuhan city or Hubei Province, China; OR ii. Been to a hospital in mainland China; OR iii. Had close contact[a] with a case of 2019 novel coronavirus infection.
February 4, 2020	(a) A person with clinical signs and symptoms suggestive of <u>pneumonia</u> or <u>severe respiratory infection with breathlessness</u> AND travel to mainland China within 14 days before onset of illness; or (b) A person with an <u>acute respiratory illness of any degree of severity</u> who, within 14 days before onset of illness had: i. Been to Hubei Province (including Wuhan city) or Zhejiang ii. Province (including Hangzhou city), China; OR iii. Been to a hospital in mainland China; OR iv. Had close contact[a] with a case of 2019 novel coronavirus infection; OR v. Had frequent or close contact during work[b] with recent travellers from mainland China (travel history in the last 14 days).
February 23, 2020	a) A person with clinical signs and symptoms suggestive of pneumonia or severe respiratory infection with breathlessness AND within 14 days before onset of illness had: i. Been to mainland China; OR ii. Been to Daegu City or Cheongdo County, South Korea. b) A person with an acute respiratory illness of any degree of severity who, within 14 days before onset of illness had: i. Been to Hubei Province (including Wuhan city) or Zhejiang Province (including Hangzhou city), China; OR ii. Been to a hospital in mainland China; OR iii. Had close contact[a] with a case of Covid-19 infection.
March 3, 2020	a) A person with clinical signs and symptoms suggestive of pneumonia or severe respiratory infection with breathlessness AND who within 14 days before onset of illness had travelled to affected areas[c]. b) A person with an acute respiratory illness of any degree of severity who, within 14 days before onset of illness had: i. Been to Hubei Province (including Wuhan city), China, Daegu city or Cheongdo County, Republic of Korea; OR ii. Been to a hospital in affected areas[c]; OR iii. Had close contact[a] with a case of Covid-19 infection.
March 9, 2020	a) A person with clinical signs and symptoms suggestive of pneumonia or severe respiratory infection with breathlessness AND who within 14 days before onset of illness had travelled abroad (i.e. to any country outside of Singapore). b) A person with an acute respiratory illness of any degree of severity who, within 14 days before onset of illness had: i. Been to any of the areas requiring heightened vigilance[d] as listed on the Healthcare Professionals Portal: https://www.moh.gov.sg/hpp/all-healthcare-professionals; OR ii. Been to any hospital abroad; OR Close contact[e] with a case of Covid-19 infection.
March 19, 2020	a) A person with clinical signs and symptoms suggestive of pneumonia or severe respiratory infection with breathlessness AND who within 14 days before onset of illness had travelled abroad (i.e. to any country outside of Singapore). b) A person with an acute respiratory illness of any degree of severity who, within 14 days before onset of illness had: i. Been to any of the areas requiring heightened vigilance[f] as listed on the Healthcare Professionals Portal: https://www.moh.gov.sg/hpp/all-healthcare-professionals; OR ii. Been to any hospital abroad; OR Close contact[e] with a case of Covid-19 infection.

7 [a] Close contact is defined as anyone who provided care for the patient, including a health care worker or family
8 member, or who had other similarly close physical contact, or anyone who stayed (e.g. lived with, visited) at the
9 same place as a case

10   [b] Persons who attended business meetings/ discussions, frontline staff in hospitality and tourism (e.g. hotels,
11   shops, tours) with regular dealings with travelers from mainland China

12   [c] Refers to affected areas with high disease load or high connectivity to Singapore. As of 3 March 2020, these
13   are: Mainland China, Republic of Korea, Japan, Northern Italy (including Milan and Venice) and Iran.

14   [d] Refers to affected areas with high disease load or high connectivity to Singapore. As of March 9, 2020, these
15   are: Mainland China, Republic of Korea, Italy, Iran, France, Germany, Spain, Japan and the United Kingdom.

16   [e] Close contact is defined as anyone who provided care for the patient, including a health care worker or family
17   member, or who had other similarly close physical contact; anyone who stayed (e.g. household members) at the
18   same place as a case; anyone who had close (i.e. less than 2m) and prolonged contact (30 min or more) with a
19   case (e.g. shared a meal)

20   [f] Refers to affected areas with high disease load or high connectivity to Singapore. As of March 19, 2020, these
21   are: Mainland China, Republic of Korea, Japan, Indonesia, Philippines, Thailand, France, Germany, Italy, Spain,
22   Switzerland, United Kingdom, United States and Iran.

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28 **Epidemiological risk factor and seroprevalence determination**

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30 **Table S2. Questionnaire for exposure risk assessment of close contacts of known Covid-19 cases.**

Data collector details	
Name of data collector	Specify name
Date of interview with contact	Specify date (DD/MM/YYYY)
Section 1. Demographic information	
Participant Study ID	Specify study ID
Age	Specify number of years
Gender	☐ Male ☐ Female
Nationality	☐ Singaporean/ Permanent resident ☐ Malaysian ☐ Chinese ☐ Filipino ☐ Indonesian ☐ Others (specify: _____)
Ethnicity	☐ Chinese ☐ Malay ☐ Indian ☐ Others (specify: _____)
Section 2. Covid-19 status	
Were you ever tested for Covid-19?	☐ Yes ☐ No
If Yes (to previous question), were any of your result positive?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify:	Date of admission to hospital in (DD/MM/YYYY) Date of discharge from isolation in (DD/MM/YYYY) Name of hospital/ isolation facility
Section 3. Relationship with known Covid-19 case(s)	
How many *known Covid-19 cases* have you had contact with?	Specify number of cases (minimum 1)
Are you a family member (i.e. spouse, child, parent, grandparent, grandchild or sibling) of any of the *known Covid-19 case(s)*?	☐ Yes ☐ No
Please specify relationship:	☐ Spouse ☐ Child ☐ Parent ☐ Grandparent ☐ Grandchild ☐ Domestic helper ☐ Fiancé(e)/ partner ☐ Sibling ☐ Relative ☐ Others: (specify: _____)
Do you share the same home/ residence as any of the *known Covid-19 case(s)?*	☐ Yes ☐ No
If Yes (to previous question), do you share the same bedroom?	☐ Yes ☐ No
Are you a colleague (same company) of any of the *known Covid-19 case(s)*?	☐ Yes (specify company name: ____) ☐ No
Do you share the same workplace building/ site as any of the *known Covid-19 case(s)*?	☐ Yes (specify location name: ____) ☐ No
Did you attend the same work-related conference/ meeting together with any of the *known Covid-19 case(s)* **who were *not* from the same company/ institution**?	☐ Yes (specify same of event: ____) ☐ No
Do you teach/ work at same childcare/ pre-school as any of the *known Covid-19 case(s)*?	☐ Yes (specify location name: ____) ☐ No
Do you teach at or attend the same school/ academic institution as any of the *known Covid-19 case(s)*?	☐ Yes (specify name of school/ institution: ____) ☐ No
Do you teach at or attend the same class (**all academic, co-curricular or non-academic type eg. karaoke class**) as any of the *known Covid-19 case(s)*?	☐ Yes ☐ No
If Yes (to previous question), please specify type of class (Select all that apply):	☐ Academic; classroom setting ☐ Academic; lecture hall setting ☐ Karaoke class ☐ Others (specify: _____)
Do you attend the same religious gathering (eg. Church) as any of the *known Covid-19 case(s)?*	☐ Yes (specify gathering: ____) ☐ No

Section 4. Exposure with known Covid-19 case(s) **from 2 weeks before start of quarantine until end of quarantine/ isolation (if hospitalized for Covid-19)**	
Quarantine start date	Specify date (DD/MM/YYYY); "NA" if not quarantined
Quarantine end date	Specify date (DD/MM/YYYY); if hospitalized due to Covid-19, quarantine end date is the same as hospital admission date; "NA" if not quarantined
Where did you come into contact with the *known Covid-19 case(s)*? Select all that apply.	☐ In a private home/ residence, may or may not be own ☐ Office (indoor workplace) ☐ Worksite (outdoor worksite) ☐ Restaurant or F&B location ☐ Hospital or clinic ☐ Hotel ☐ Retail location ☐ Indoor gym or fitness class ☐ Place of worship ☐ Entertainment venue (eg. club, karaoke lounge etc.) ☐ Others (specify: _____)
Largest number of persons present when you had contact (including you and the *known Covid-19 case(s)*)	Specify number of persons (minimum 2)
Smallest number of persons present when you had contact (including you and the *known Covid-19 case(s)*)	Specify number of persons (minimum 2)
Was the *known Covid-19 case(s)* visibly unwell/ known to be unwell at any point during this two-week period?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify noted/ known symptoms (select all that apply):	☐ Fever (measured temperature of 38ºC or higher) ☐ Cough ☐ Sore throat ☐ Shortness of breath ☐ Runny and/or blocked nose ☐ Diarrhoea ☐ Abdominal discomfort ☐ Muscle ache ☐ Fatigue ☐ Others (specify:)
Did you provide care for the *known Covid-19 case(s)*?	☐ Yes ☐ No
If Yes (to previous question), were you a healthcare worker attending to the known Covid-19 case(s)?	☐ Yes ☐ No
Was the *known Covid-19 case(s)* wearing a mask during **all** the episodes of contact?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify type of mask (select all that apply):	☐ Surgical mask ☐ N95 respirator ☐ Other types (eg. cloth)
Were you wearing a mask during **all** the episodes of contact?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify type of mask (select all that apply):	☐ Surgical mask ☐ N95 respirator ☐ Other types (eg. cloth)
Were you in the same room or enclosed venue as the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Were you in the same vehicle as the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify type of vehicle (select all that apply):	☐ Car ☐ Others (specify:)
Describe the closest physical distance shared with the *known Covid-19 case(s)* to the nearest metre.	Specify number of meters (Indicate direct contact as 0)
Did you have direct physical contact with the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify type of direct contact (select all that apply):	☐ Kissing ☐ Hugging ☐ Hand-to-hand contact (eg. shaking hands, holding hands) ☐ Others (specify:)
Did the *known Covid-19 case(s)* hand over any objects directly to you/ Did you touch any surfaces immediately after the *known Covid-19 case(s)?*	☐ Yes ☐ No ☐ Don't know

If Yes (to previous question), please specify type of object (select all that apply):	☐ Microphone ☐ Money/ credit card(s) ☐ Exposed food/ drink items ☐ Serving spoon/utensils/ dinnerware ☐ Mobile phone ☐ Computer keyboard/ mouse ☐ Pen/ other writing tools ☐ Others (specify:_____)
Did you share a meal at the same table with the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did you eat from the same plate as the *known Covid-19 case(s)* (including communal serving plates)?	☐ Yes ☐ No ☐ Don't know
Did you drink from the same drinking cup/ glass with the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did you eat from the same utensils with the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did you knowingly use the same toilet after the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did you share or have access to the same toilet as the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did you use the same microphone with the *known Covid-19 case(s)*?	☐ Yes ☐ No ☐ Don't know
Did any of the *known Covid-19 case(s)* sing during any contact episode?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify:	Shortest distance apart (in number of meters, rounded up to nearest meter) Duration of the longest singing episode (in number of minutes, rounded up to the nearest minute)
Did the *known Covid-19 case(s)* speak to you (including addressing a group you are part of)?	☐ Yes ☐ No ☐ Don't know
If Yes (to previous question), please specify:	Largest number of persons present in same room during speaking episode (including you and the *known Covid-19 case(s);* minimum 2) Duration of the longest speaking episode (in number of minutes, rounded up to the nearest minute)
Section 5. Symptoms during the period defined as: **from 2 weeks before start of quarantine or until end of quarantine/ isolation (if hospitalized for Covid-19)**	
Did you develop any symptoms after the **first contact** with the *known Covid-19 case(s)* **during the defined period?**	☐ Yes ☐ No
If Yes (to previous question), please specify:	Date of onset of symptoms (DD/MM/YYYY) Type of symptoms (select all that apply): ☐ Fever (measured temperature of 38ºC or higher) ☐ Cough ☐ Sore throat ☐ Shortness of breath ☐ Runny and/or blocked nose ☐ Diarrhoea ☐ Abdominal discomfort ☐ Muscle ache ☐ Fatigue ☐ Others (specify:_____)
Did all symptoms resolve?	☐ Yes ☐ No
If Yes (to previous question), specify date when all symptoms resolved	Specify date (DD/MM/YYYY)
Section 6. Medical History	
Have you been previously diagnosed with SARS/ MERS?	☐ Yes ☐ No
Do you have any chronic medical conditions?	☐ Yes ☐ No
If Yes (to previous question), specify type of condition(s) (select all that apply)	☐ Diabetes ☐ Hypertension ☐ Heart disease ☐ Stroke ☐ Others (specify:_____)

Were you taking any medications for diabetes/ hypertension/ heart disease/ stroke **from 2 weeks before start of quarantine or until end of quarantine/ isolation (if hospitalized for Covid-19)**?	☐ Yes (specify: _____) ☐ No
Were you taking any anti-inflammatory or pain medications **from 2 weeks before start of quarantine or until end of quarantine/ isolation (if hospitalized for Covid-19)?**	☐ Yes (specify: _____) ☐ No
Section 7. Travel History	
Have you travelled to Wuhan, China since 01/12/2019?	☐ Yes ☐ No
If Yes (to previous question), please specify period of travel:	DD/MM/YYYY to DD/MM/YYYY
Have you travelled to China (other than Wuhan) since 01/12/2019?	☐ Yes ☐ No
If Yes (to previous question), please specify period of travel:	DD/MM/YYYY to DD/MM/YYYY
Have you travelled abroad (to countries other than China) since 01/12/2019?	☐ Yes ☐ No
If Yes (to previous question), please specify:	Name of country (select all that apply): ☐ Malaysia ☐ Indonesia ☐ Philippines ☐ South Korea ☐ Japan ☐ United Kingdom ☐ United States of America ☐ Italy ☐ Spain ☐ Germany ☐ France ☐ Others (specify: _____) Period for each country: (DD/MM/YYYY to DD/MM/YYYY)

Serological methods and assay thresholds

A SARS-CoV-2 surrogate virus neutralization test (sVNT) based on antibody-mediated blockage of ACE2-spike protein-protein interaction was used. Briefly, human ACE-2 (hACE2) protein (Genscript Biotech, New Jersey, United States) was coated at 100 ng/well in 100 mM carbonate-bicarbonate coating buffer (pH 9.6). 3 ng of horseradish peroxidase (HRP)-conjugated recombinant receptor binding domain (RBD) from the spike protein of SARS-CoV-2 (GenScript Biotech) was pre-incubated with test serum at the final dilution of 1:20 for 1 hour at 37°C, followed by hACE2 incubation for 1 h at room temperature. Unbound HRP-conjugated SARS-CoV-2 RBD was removed by five washes using phosphate buffered saline with 0.05% tween-20. The colorimetric signal was developed on the enzymatic reaction of HRP with chromogenic substrate, 3,3',5,5'-tetramethylbenzidine (Invitrogen, California, United States). Equal volume of TMB stop solution (Kirkegaard & Perry Laboratories, Maryland, United States) was added to stop the reaction, and the absorbance reading (OD) at 450 nm and 570 nm were acquired using Cytation 5 microplate reader (BioTek, Vermont, United States). Inhibition (%) = (1 - Sample OD value/ Negative Control OD value) x100.

A positive serological test result was concluded if the sVNT for a particular sample resulted in inhibition of 30% or greater (98.9% sensitivity and 100% specificity), as previously validated by Tan and colleagues[1].

Co-variate analysis for secondary clinical attack rates

On multivariate logistic regression to relate secondary clinical attack rate to age, gender, symptom duration and group, after adjusting for interactions, younger aged (<30) contacts had lower risk than those aged over 50 (aOR 0.52, 95% CI 0.35–0.78; p=0.0014). Work and social contacts also were at significantly lower risk than household contacts (social: aOR 0.34, 95% CI 0.17–0.65; p=0.0015; work: aOR 0.09, 95% CI 0.03–0.25; p<0.0001). The interaction term between male sex and work is significant.

Table S3A. Co-variate analysis for secondary clinical attack rate.

	Attack rate	aOR	95%CI		p
Overall					
Male	0.025	1.24	(0.83,	1.58)	0.30
Female	0.023	1 (REF)			
Age <30	**0.015**	**0.52**	**(0.35,**	**0.78)**	**0.0014**
Age 30–49	0.029	1.11	(0.78,	1.60)	0.55
Age 50+	0.031	1 (REF)			
Symptom Duration		1	(0.95,	1.06)	0.88
Social	**0.059**	**0.34**	**(0.17,**	**0.65)**	**0.0015**
Work	**0.013**	**0.09**	**(0.03,**	**0.25)**	**<0.0001**
Household	0.013	1 (REF)			
Male x Work		**2.93**	**(1.15,**	**8.51)**	**0.032**
Male x Social		0.76	(0.37,	1.56)	0.46
Male x Household		1 (REF)			
Symptom Duration x Work		1.00	(0.88,	1.13)	0.99
Symptom Duration x Social		0.94	(0.84,	1.04)	0.24
Symptom Duration x Household		1 (REF)			

The significant interaction between sex and type of contact is clarified through the comparisons in Table S3B.

Table S3B. Co-variate analysis for secondary clinical attack rate: interactions with sex and contact type.

Among	Odds of secondary clinical infection between:	aOR	95%CI		p
Males:	**Work vs Household**	**0.26**	**(0.11,**	**0.59)**	**0.0014**
	Social vs Household	**0.26**	**(0.13**	**0.53)**	**0.0002**
Females	**Work vs Household**	**0.09**	**(0.03**	**0.26)**	**<0.0001**
	Social vs Household	**0.34**	**(0.17**	**0.66)**	**0.0015**
Household contacts	Male vs female	1.24	(0.83	1.85)	0.29
Social contacts	Male vs female	0.94	(0.52	1.72)	0.86
Work contacts	**Male vs female**	**3.63**	**(1.48**	**8.94)**	**0.0049**

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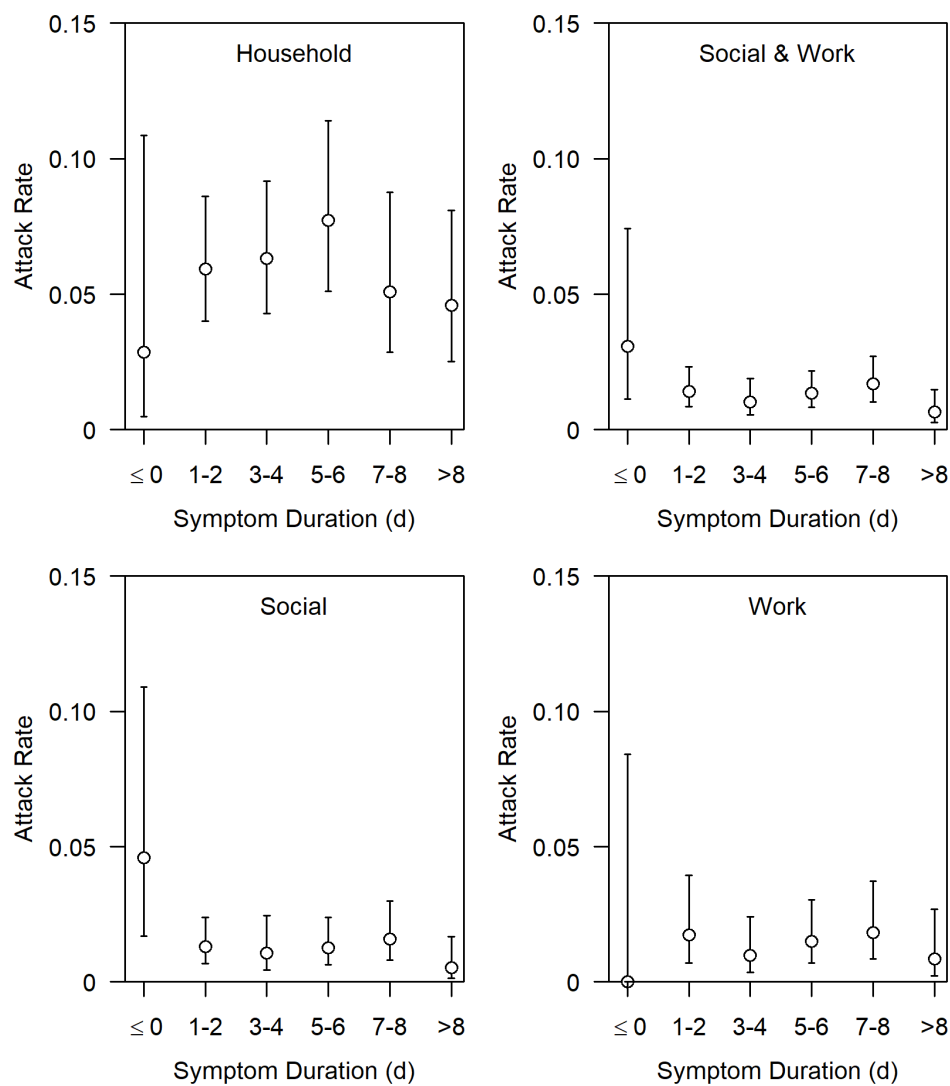
70 **Figure S1.** Attack rate by symptom duration of index case prior to hospitalization, in number of days.

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Clustering in secondary attack rates

We tested for clustering in secondary attack rates within location types by fitting binomial models, which assume independent outcomes for each contact, and beta-binomial models, which allow for over-dispersion relative to a binomial model, and reduce to the binomial in the special case where the two parameters tend to infinity. The parameters for the two model classes were estimated using maximum likelihood estimation. The two models were compared by the likelihood ratio test, with the difference in twice the log-likelihood at the maximum likelihood value being distributed as a chi-squared with one degree of freedom, if the binomial model were true.

Differences in participation rate for serology

We assess whether there were differences in the profile of contacts who participated in the serology component of the study and those who declined to through logistic regressions within location types.

For household contacts, past PCR sampling was not significantly associated with consenting for serology and questionnaire (OR 0.80; p=0.067). Age and gender of the contact were also not significant predictors of participation in serology (p=0.18 and 0.95, respectively) in household members.

Among social contacts, older individuals were substantially more likely to seek serologic confirmation of infection (OR 1.13 per decade, 95% CI 1.08—1.19; p<0.0001). Neither sex nor past PCR sampling were significant (p=0.55 and 0.33, respectively).

Among work contacts, nothing was associated with undertaking serology (sex, p=0.29; age, p=0.86; PCR, p=0.14).

Bayesian analysis

To estimate the overall infection rate and asymptomatic proportion, we partition contacts into nine groups with sixteen subgroups as tabulated in **Table S4** and illustrated in **Figure S2**.

Table S4. Definition of grouping of contacts. Colours correspond to those in Figure S2.

A	A	Were symptomatic, tested by PCR and tested positive
BL		Were symptomatic, tested by PCR and tested negative, did not come forward for serology and were:
	B	actually infected (false negative on PCR)
	L	truly uninfected
C	C	Were symptomatic, tested by PCR and tested negative, came forward for serology and tested positive
DK		Were symptomatic, tested by PCR and tested negative, came forward for serology and tested negative, and were:
	D	actually infected (false negative on both PCR and serology)
	K	truly uninfected
E	E	Were symptomatic, avoided testing by PCR, came forward for serology and tested positive
FM		Were symptomatic, avoided testing by PCR, came forward for serology, tested negative, and were:
	F	actually infected (false negative on serology)
	M	truly uninfected
GJNP		Did not do PCR or serology and were:
	G	actually infected and symptomatic
	J	actually infected but asymptomatic
	N	uninfected but symptomatic with another pathogen
	P	uninfected and asymptomatic
H	H	Were asymptomatic, came forward for serology and tested positive
IO		Were asymptomatic, came forward for serology, tested negative and were:
	I	actually infected (false negative on serology)
	O	truly uninfected

If we define the following parameters:

$$\pi = P(\text{infected})$$

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$$s = P(\text{symptomatic} \mid \text{infected})$$
$$y = P(\text{symptomatic} \mid \text{uninfected})$$
$$p = P(\text{tested with PCR} \mid \text{symptomatic})$$
$$v = P(\text{PCR positive} \mid \text{tested and infected})$$
$$\sigma = P(\text{Seropositive} \mid \text{tested and infected})$$
$$\tau = P(\text{tested with serology} \mid \text{not PCR positive})$$

then the probabilities of an individual falling into any of these groups are given in **Table S5**.

Figure S2. Logic diagram for the Bayesian model.
Labelled large circles correspond to subgroups, with colours (excluding black) indicating which fall within the same group. Red circles: subgroups B and L had symptoms but were PCR negative (either a true negative or false negative) and did not have serology. Green circles: subgroups D and K had symptoms but were PCR negative (ditto), went for serology and were seronegative (ditto). Pink circles: subgroups F and M had symptoms but missed PCR testing, went for serology and were seronegative (ditto). Orange circles: subgroups G, J, N, and P did not undergo PCR or serology testing (and may or may not have been infected or symptomatic). Blue circles: subgroups I and O were not symptomatic, went for serology and were seronegative (either a true negative or false negative). Black (large) circles are those whose status are not indeterminate. Small black circles correspond to questions in the x axis. Arrows represent yes (blue) and no (red) answers to those questions. Parameters indicate the probability of a yes or no answer.

Group	Sub-group	Probability of subgroup	Count (home)	Count (social)	Count (work)	Count (all)
A	A	πspv	110	47	31	188
BL	B	$\pi sp(1-v)(1-\tau)$	273	374	278	925
BL	L	$(1-\pi)yp(1-\tau)$	-	-	-	-
C	C	$\pi sp(1-v)\tau\sigma$	5	2	2	9
DK	D	$\pi sp(1-v)\tau(1-\sigma)$	106	58	35	199
DK	K	$(1-\pi)yp\tau$	-	-	-	-
E	E	$\pi s(1-p)\tau\sigma$	7	2	1	10
FM	F	$\pi s(1-p)\tau(1-\sigma)$	20	20	15	55
FM	M	$(1-\pi)y(1-p)\tau$	-	-	-	-
GJNP	G	$\pi s(1-p)(1-\tau)$	956	2748	1803	5507
GJNP	J	$\pi(1-s)(1-\tau)$	-	-	-	-
GJNP	N	$(1-\pi)y(1-p)(1-\tau)$	-	-	-	-
GJNP	P	$(1-\pi)(1-y)(1-\tau)$	-	-	-	-
H	H	$\pi(1-s)\tau\sigma$	17	5	3	25
IO	I	$\pi(1-s)\tau(1-\sigma)$	369	332	151	852
IO	O	$(1-\pi)(1-y)\tau$	-	-	-	-

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132 The likelihood for the number of people in each group,

133 $$\{n_A, n_{BL}, n_C, n_{DK}, n_E, n_{FM}, n_{GJNP}, n_H, n_{IO}\},$$

134 follows from a multinomial mass function. A beta prior is adopted to encapsulate the information on the
135 serologic sensitivity parameter from 175 PCR confirmed cases of whom 173 tested positive at the threshold
136 used to determine seropositivity, specifically $\sigma \sim Be(174,3)$. This choice of prior propagates uncertainty from
137 the previous study by Tan and colleagues[1] to the current study. We did not consider sensitivity of the findings to
138 prior distributions that clashed with the information from Tan and colleagues' study. All other parameters are
139 given $U(0,1)$ priors; we similarly did not assess the value of using informative priors for these other parameters
140 since the posterior distributions were informative based on the data alone.

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142 The model is fit to each group of contacts (household, work and social) and all three groups combined. The data
143 used are tabulated in **Supplementary Table S5**. The probability of a contact being infected and that infection
144 being missed by symptom-based PCR was defined to be $\pi - \pi spv = \pi(1 - spv)$, and the proportion of
145 infections that were missed was therefore $1 - spv$. The asymptomatic to symptomatic ratio was $(1 - s)/s$.

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147 The model was fit using Markov chain Monte Carlo with 100 000 iterations; pilot runs were used to tune the
148 initial conditions (i.e. serving as burn-in, so the initial conditions are already a draw from the posterior) and
149 variances for the proposal distribution. R code is available as Supplementary Code. Convergence was checked
150 through trace plots (presented in Figures S6–12). Posteriors for the parameters are tabulated in **Table S6**;
151 derived estimates (the proportion asymptomatic, asymptomatic to symptomatic ratio, proportion of infections
152 missed by symptom-based PCR, and the probability of being infected yet not identified) are presented in **Table**
153 **S7**.

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155 **Table S6. Posterior mean and 95% equal-tailed credible intervals in parenthesis for model parameters by**
156 **contact type (home, social, work or all types).**

|	Definition	Home	Social	Work	All
π	Probability of infection	0.11 (0.09, 0.14)	0.04 (0.03, 0.05)	0.05 (0.03, 0.08)	0.06 (0.05, 0.08)
s	Probability of symptoms if infected	0.72 (0.62, 0.82)	0.65 (0.45, 0.84)	0.64 (0.40, 0.87)	0.64 (0.55, 0.73)
p	Probability of getting PCR if symptomatic	0.84 (0.79, 0.89)	0.71 (0.63, 0.79)	0.65 (0.54, 0.75)	0.75 (0.70, 0.79)
v	Probability of testing positive on PCR if infected	0.85 (0.74, 0.94)	0.75 (0.52, 0.93)	0.66 (0.41, 0.90)	0.79 (0.68, 0.88)
τ	Probability of getting serology	0.30 (0.28, 0.32)	0.12 (0.11, 0.13)	0.09 (0.08, 0.10)	0.15 (0.14, 0.16)
σ	Probability of testing positive on serology if infected	0.98 (0.96, 1.00)	0.98 (0.96, 1.00)	0.98 (0.96, 1.00)	0.98 (0.96, 1.00)
y	Probability of symptoms if uninfected	0.26 (0.24, 0.29)	0.17 (0.15, 0.19)	0.21 (0.18, 0.25)	0.20 (0.18, 0.22)

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160 **Table S7. Posterior mean and 95% equal-tailed credible intervals in parenthesis.**

|	Definition	Home	Social	Work	All
$\pi(1-spv)$	Probability of being infected and that infection being missed by symptom-based PCR	0.06 (0.04, 0.07)	0.03 (0.01, 0.04)	0.04 (0.02, 0.06)	0.04 (0.03, 0.05)
$1-spv$	Proportion of infections missed by symptom-based PCR	0.48 (0.39, 0.57)	0.66 (0.52, 0.77)	0.73 (0.58, 0.84)	0.62 (0.55, 0.69)
$(1-s)/s$	Asymptomatic to symptomatic ratio	0.39 (0.23, 0.62)	0.58 (0.20, 1.20)	0.61 (0.15, 1.47)	0.57 (0.36, 0.83)
$(1-s)$	Asymptomatic proportion	0.28 (0.18, 0.38)	0.35 (0.16, 0.55)	0.36 (0.13, 0.60)	0.36 (0.27, 0.45)

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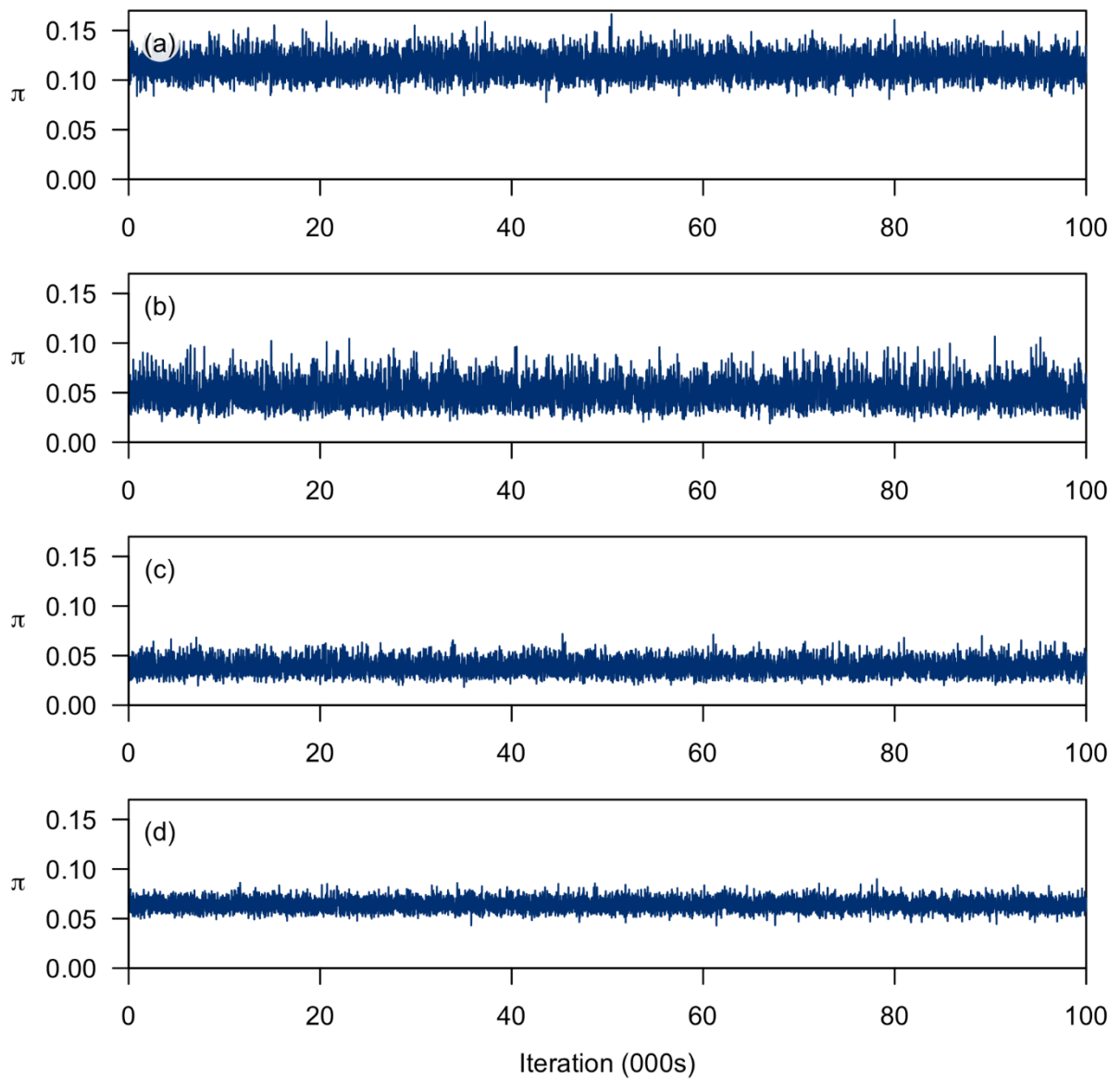
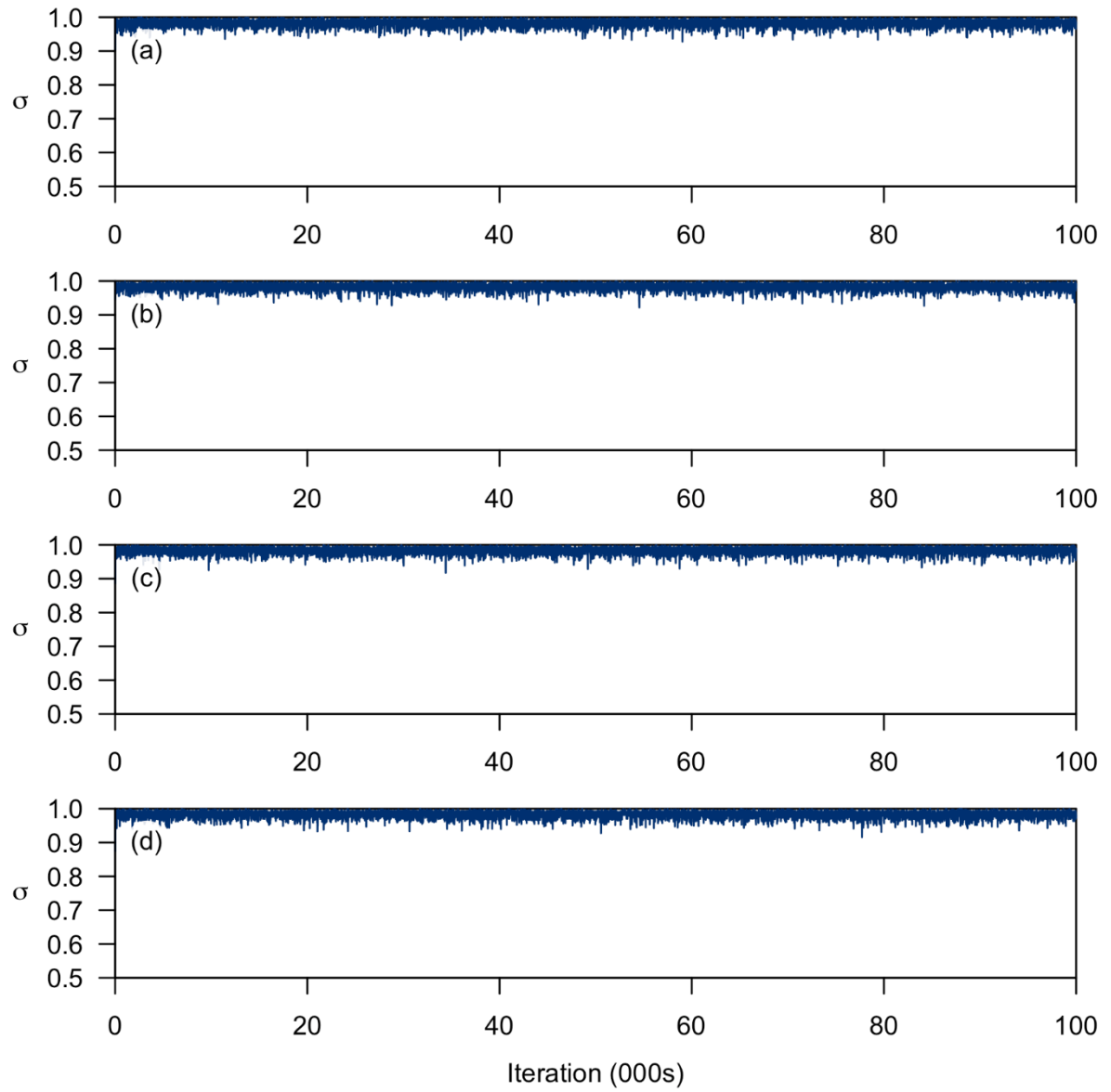**Figure S6. Traceplots for π for home (a), work (b), social (c) and all (d) contacts.**
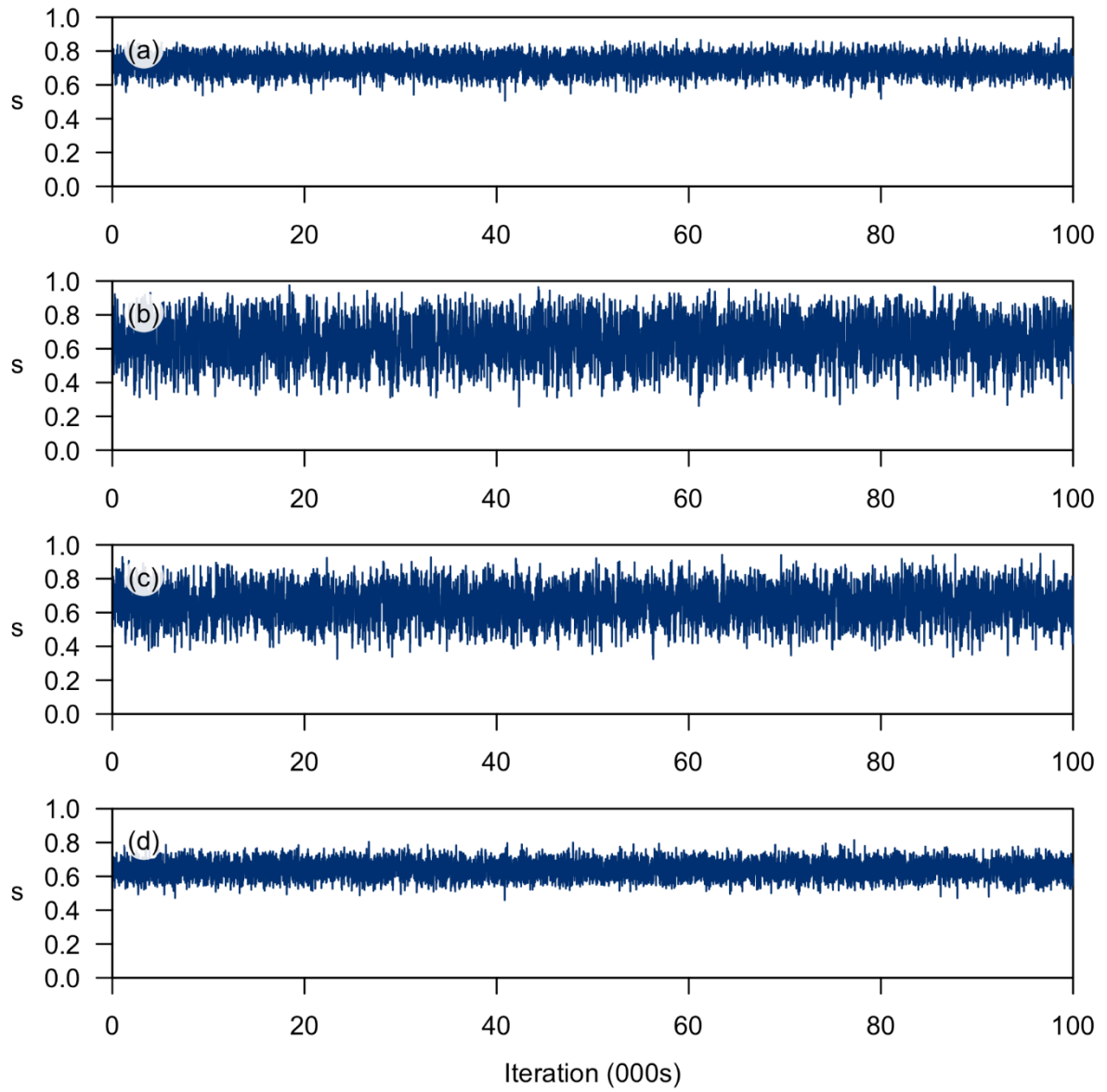
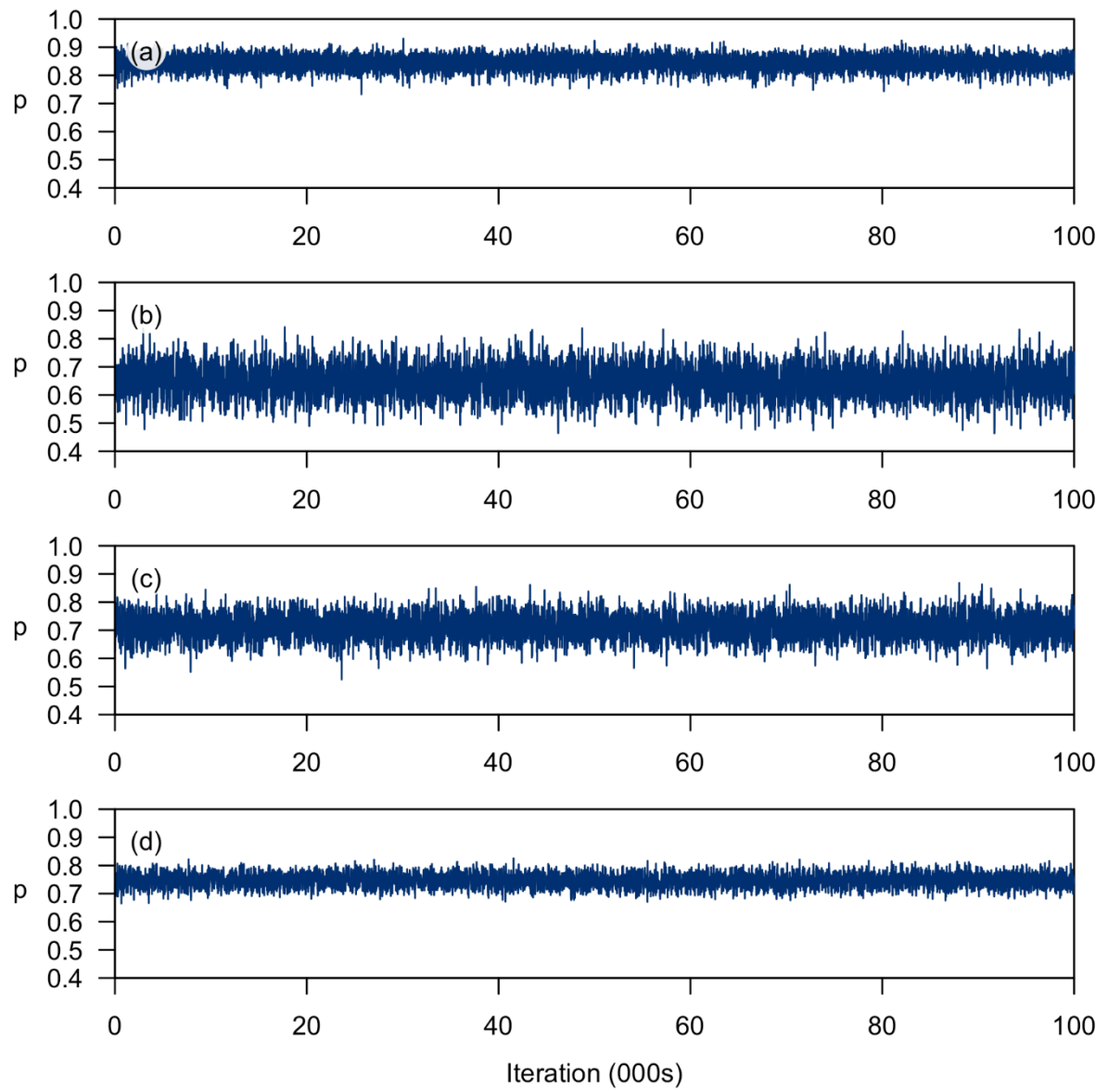**Figure S7. Traceplots for *s* for home (a), work (b), social (c) and all (d) contacts.**
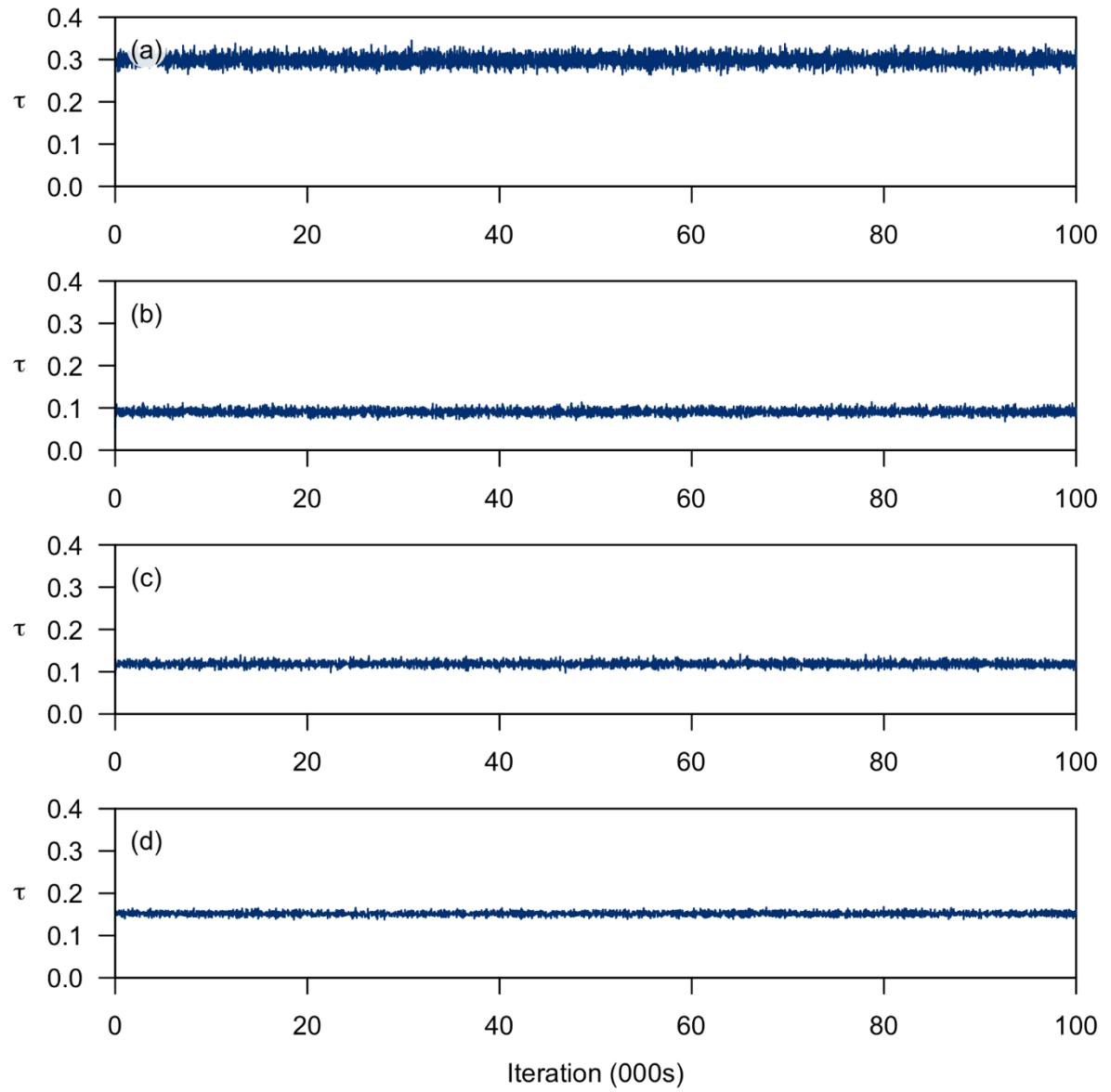
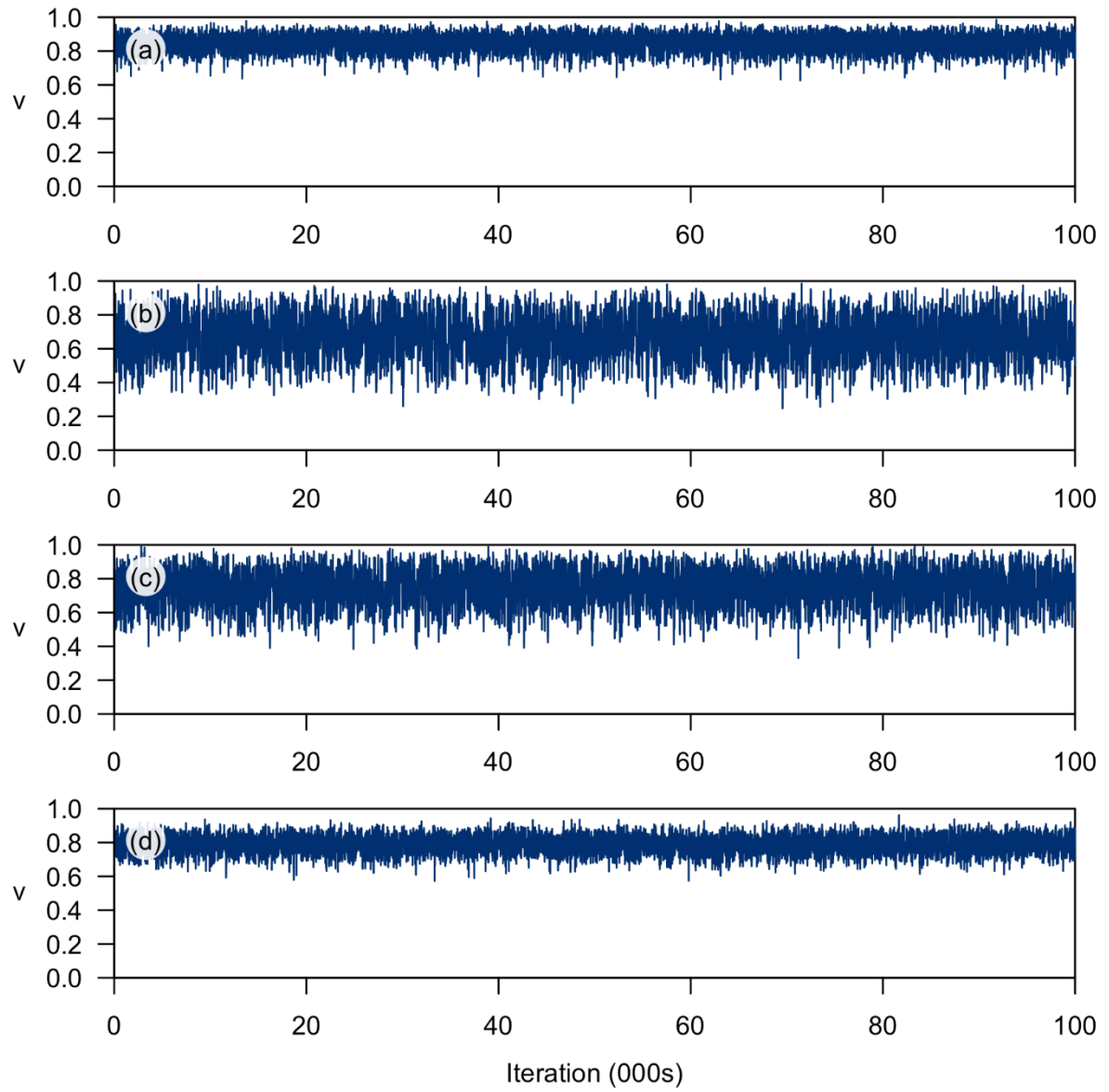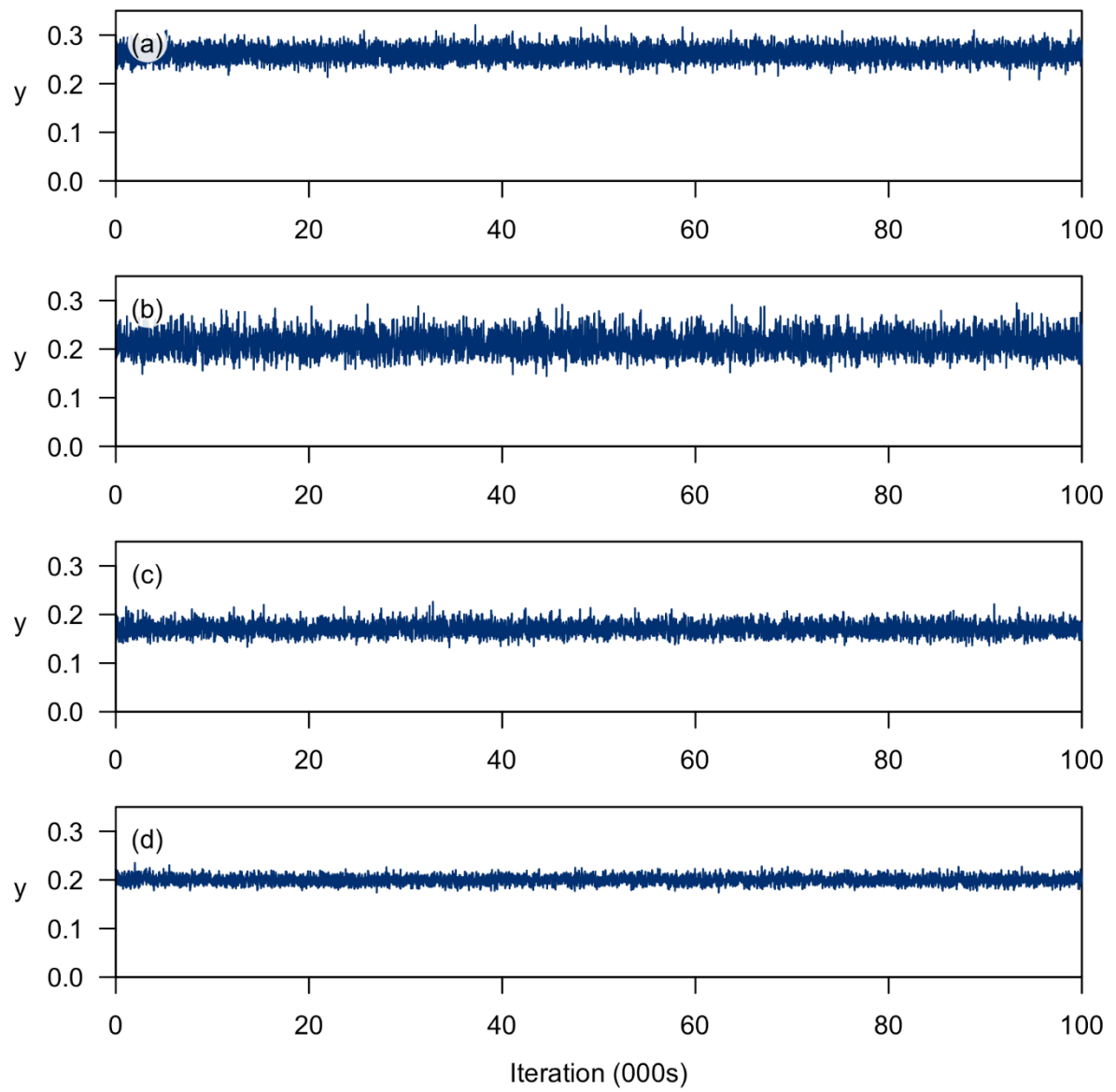**Figure S8. Traceplots for τ for home (a), work (b), social (c) and all (d) contacts.**

Figure S9. Traceplots for σ for home (a), work (b), social (c) and all (d) contacts.

Figure S10. Traceplots for p for home (a), work (b), social (c) and all (d) contacts.

Figure S11. Traceplots for v for home (a), work (b), social (c) and all (d) contacts.

Figure S12. Traceplots for y for home (a), work (b), social (c) and all (d) contacts.

R code for the MCMC

```r
# dir.create('mcmc') # unless there's already a subdirectory by that name in the working directory

ps = function(pars)
{
 q=pars
 p_a   = q$pi*q$s*q$p*q$v
 p_e   = q$pi*q$s*(1-q$p)*q$tau*q$sigma
 p_fm  = q$pi*q$s*(1-q$p)*q$tau*(1-q$sigma) + (1-q$pi)*q$y*(1-q$p)*q$tau
 p_gjnp= q$pi*q$s*(1-q$p)*(1-q$tau) + (1-q$pi)*q$y*(1-q$p)*(1-q$tau)+ q$pi*(1-q$s)*(1-q$tau) + (1-
q$pi)*(1-q$y)*(1-q$tau)
 p_h   = q$pi*(1-q$s)*q$tau*q$sigma
 p_io  = q$pi*(1-q$s)*q$tau*(1-q$sigma) + (1-q$pi)*(1-q$y)*q$tau
 p_dk  = (1-q$pi)*q$y*q$p*q$tau + q$pi*q$s*q$p*(1-q$v)*q$tau*(1-q$sigma)
 p_bl  = (1-q$pi)*q$y*q$p*(1-q$tau) + q$pi*q$s*q$p*(1-q$v)*(1-q$tau)
 p_c   = q$pi*q$s*q$p*(1-q$v)*q$tau*q$sigma
 return(c(p_a,p_e,p_fm,p_gjnp,p_h,p_io,p_dk,p_bl,p_c))
}

logl_ALL = function(pars)
{
 ns <- c(188L, 10L, 55L, 5507L, 25L, 852L, 199L, 925L, 9L)
 pars$LL = dmultinom(ns,prob=ps(pars),log=TRUE)+dbeta(pars$sigma,173+1,2+1,log=TRUE)
 return(pars)
}

logl_HH = function(pars)
{
 ns <- c(110L, 7L, 20L, 956L, 17L, 369L, 106L, 273L, 5L)
 pars$LL = dmultinom(ns,prob=ps(pars),log=TRUE)+dbeta(pars$sigma,173+1,2+1,log=TRUE)
 return(pars)
}

logl_WORK = function(pars)
{
 ns <- c(31L, 1L, 15L, 1803L, 3L, 151L, 35L, 278L, 2L)
 pars$LL = dmultinom(ns,prob=ps(pars),log=TRUE)+dbeta(pars$sigma,173+1,2+1,log=TRUE)
 return(pars)
}

logl_SOC = function(pars)
{
 ns <- c(47L, 2L, 20L, 2748L, 5L, 332L, 58L, 374L, 2L)
 pars$LL = dmultinom(ns,prob=ps(pars),log=TRUE)+dbeta(pars$sigma,173+1,2+1,log=TRUE)
 return(pars)
}




mh=function(oldpars,newpars)
{
 reject=FALSE
 if(newpars$pi<0)reject=TRUE
 if(newpars$pi>1)reject=TRUE
 if(newpars$tau<0)reject=TRUE
 if(newpars$tau>1)reject=TRUE
 if(newpars$s<0)reject=TRUE
 if(newpars$s>1)reject=TRUE
```

```
  if(newpars$sigma<0)reject=TRUE
  if(newpars$sigma>1)reject=TRUE
  if(newpars$p<0)reject=TRUE
  if(newpars$p>1)reject=TRUE
  if(newpars$v<0)reject=TRUE
  if(newpars$v>1)reject=TRUE
  if(newpars$y<0)reject=TRUE
  if(newpars$y>1)reject=TRUE
  if(!reject)
  {
   newpars = logl(newpars)
   logacc = newpars$LL-oldpars$LL
   lu = -rexp(1)
   if(lu>logacc)reject=TRUE
  }
  if(reject)return(oldpars)
  return(newpars)
}


for(TYPE in c('HH','ALL','WORK','SOC'))
{
 cat('Type:',TYPE,'\n')
 if(TYPE=='HH')logl=logl_HH
 if(TYPE=='ALL')logl=logl_ALL
 if(TYPE=='WORK')logl=logl_WORK
 if(TYPE=='SOC')logl=logl_SOC


 pars = list(pi=0.1,s=0.6,p=0.9,tau=0.3,sigma=0.9,y=0.4,v=0.95)
 proposalsd = list(pi=0.01,s=0.05,p=0.1,tau=0.1,sigma=0.01,y=0.05,v=0.05)

 input_file = paste0('mcmc/mcmc_extended_',TYPE,'.csv')
 if(file.exists(input_file))
 {
  lastrun = read.csv(input_file)
  N = dim(lastrun)[1]
  pars$pi    = lastrun$pi[N]
  pars$tau   = lastrun$tau[N]
  pars$s     = lastrun$s[N]
  pars$sigma = lastrun$sigma[N]
  pars$p     = lastrun$p[N]
  pars$y     = lastrun$y[N]
  pars$v     = lastrun$v[N]
  proposalsd$pi    = sd(lastrun$pi)
  proposalsd$tau   = sd(lastrun$tau)
  proposalsd$s     = sd(lastrun$s)
  proposalsd$sigma = sd(lastrun$sigma)
  proposalsd$p     = sd(lastrun$p)
  proposalsd$y     = sd(lastrun$y)
  proposalsd$v     = sd(lastrun$v)
  rm(input_file,N,lastrun)
 }


 pars = logl(pars)

 MCMCits = 100000
 storage =
list(pi=rep(0,MCMCits),tau=rep(0,MCMCits),s=rep(0,MCMCits),sigma=rep(0,MCMCits),p=rep(0,MCMCits),
```

```
            y=rep(0,MCMCits),v=rep(0,MCMCits))
  for(iteration in 1:MCMCits)
  {
   if(iteration%%10000==0)cat('Iteration',iteration,'of',MCMCits,'\n')

   oldpars=pars;pars$pi    = rnorm(1,pars$pi,0.01);    pars = mh(oldpars,pars)
   oldpars=pars;pars$s     = rnorm(1,pars$s,0.05);     pars = mh(oldpars,pars)
   oldpars=pars;pars$p     = rnorm(1,pars$p,0.1);      pars = mh(oldpars,pars)
   oldpars=pars;pars$tau   = rnorm(1,pars$tau,0.1);    pars = mh(oldpars,pars)
   oldpars=pars;pars$sigma = rnorm(1,pars$sigma,0.01); pars = mh(oldpars,pars)
   oldpars=pars;pars$y     = rnorm(1,pars$y,0.05);     pars = mh(oldpars,pars)
   oldpars=pars;pars$v     = rnorm(1,pars$v,0.05);     pars = mh(oldpars,pars)


   storage$pi[iteration]    = pars$pi
   storage$tau[iteration]   = pars$tau
   storage$s[iteration]     = pars$s
   storage$sigma[iteration] = pars$sigma
   storage$p[iteration]     = pars$p
   storage$y[iteration]     = pars$y
   storage$v[iteration]     = pars$v
  }

  pdf('trace.pdf')
  i=seq(10,100000,10)
  plot(storage$sigma[i])
  plot(storage$pi[i])
  plot(storage$tau[i])
  plot(storage$s[i])
  plot(storage$p[i])
  plot(storage$y[i])
  plot(storage$v[i])
  dev.off()
  storage = as.data.frame(storage)

  write.csv(storage,paste0('mcmc/mcmc_extended_',TYPE,'.csv'),row.names = FALSE)
}

rm(oldpars,pars,storage,iteration,MCMCits,TYPE)
rm(logl,logl_ALL,logl_HH,logl_SOC,logl_WORK,mh,ps)
rm(i,proposalsd)
```

References

1 Tan CW, Chia WN, Qin X, *et al.* A SARS-CoV-2 surrogate virus neutralization test based on antibody-mediated blockage of ACE2–spike protein–protein interaction. *Nat Biotechnol* 2020; published online July 23. DOI:10.1038/s41587-020-0631-z.